

## **RAW SEQUENCE LISTING**

**The Biotechnology Systems Branch of the Scientific and Technical  
Information Center (STIC) no errors detected.**

Application Serial Number: 09/807,949C  
Source: 1 Fw/6,  
Date Processed by STIC: 11/23/05

# ***ENTERED***



IFW16

## RAW SEQUENCE LISTING

DATE: 11/23/2005

PATENT APPLICATION: US/09/807,949C

TIME: 13:48:40

Input Set : A:\USSN 09-807,949-SEQ LISTING.txt

Output Set: N:\CRF4\11232005\I807949C.raw

3 <110> APPLICANT: Zavada, Jan  
 4 Pastorekova, Silvia  
 5 Pastorek, Jaromir  
 7 <120> TITLE OF INVENTION: MN Gene and Protein  
 9 <130> FILE REFERENCE: D-0021.5 PCT  
 C--> 11 <140> CURRENT APPLICATION NUMBER: US/09/807,949C  
 C--> 12 <141> CURRENT FILING DATE: 2001-08-09  
 14 <150> PRIOR APPLICATION NUMBER: 09/177,776  
 15 <151> PRIOR FILING DATE: 1998-10-23  
 17 <150> PRIOR APPLICATION NUMBER: 09/178,115  
 18 <151> PRIOR FILING DATE: 1998-10-23  
 20 <160> NUMBER OF SEQ ID NOS: 143  
 22 <170> SOFTWARE: PatentIn Ver. 2.1  
 24 <210> SEQ ID NO: 1  
 25 <211> LENGTH: 1522  
 26 <212> TYPE: DNA  
 27 <213> ORGANISM: HUMAN  
 29 <220> FEATURE:  
 30 <221> NAME/KEY: CDS  
 31 <222> LOCATION: (13)..(1389)  
 33 <220> FEATURE:  
 34 <221> NAME/KEY: mat\_peptide  
 35 <222> LOCATION: (124)..(1389)  
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 40 -35 -30 -25  
 42 atc ccg gcc cct gct cca ggc ctc act gtg caa ctg ctg ctg tca ctg 99  
 43 Ile Pro Ala Pro Ala Pro Gly Leu Thr Val Gln Leu Leu Leu Ser Leu  
 44 -20 -15 -10  
 46 ctg ctt ctg atg cct gtc cat ccc cag agg ttg ccc cgg atg cag gag 147  
 47 Leu Leu Leu Met Pro Val His Pro Gln Arg Leu Pro Arg Met Gln Glu  
 48 -5 -1 1 5  
 50 gat tcc ccc ttg gga gga ggc tct tct ggg gaa gat gac cca ctg ggc 195  
 51 Asp Ser Pro Leu Gly Gly Ser Ser Gly Glu Asp Asp Pro Leu Gly  
 52 10 15 20  
 54 gag gag gat ctg ccc agt gaa gag gat tca ccc aga gag gag gat cca 243  
 55 Glu Glu Asp Leu Pro Ser Glu Glu Asp Ser Pro Arg Glu Glu Asp Pro  
 56 25 30 35 40  
 58 ccc gga gag gag gat cta cct gga gag gag gat cta cct gga gag gag 291  
 59 Pro Gly Glu Glu Asp Leu Pro Gly Glu Glu Asp Leu Pro Gly Glu Glu  
 60 45 50 55  
 62 gat cta cct gaa gtt aag cct aaa tca gaa gaa gag ggc tcc ctg aag 339

p.6

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|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|------|
| 63  | Asp | Leu | Pro | Glu | Val | Lys | Pro | Lys | Ser | Glu | Glu | Glu | Gly | Ser | Leu | Lys |      |
| 64  |     |     |     | 60  |     |     |     |     | 65  |     |     |     |     | 70  |     |     |      |
| 66  | tta | gag | gat | cta | cct | act | gtt | gag | gct | cct | gga | gat | cct | caa | gaa | ccc | 387  |
| 67  | Leu | Glu | Asp | Leu | Pro | Thr | Val | Glu | Ala | Pro | Gly | Asp | Pro | Gln | Glu | Pro |      |
| 68  |     |     | 75  |     |     |     |     | 80  |     |     |     |     | 85  |     |     |     |      |
| 70  | cag | aat | aat | gcc | cac | agg | gac | aaa | gaa | ggg | gat | gac | cag | agt | cat | tgg | 435  |
| 71  | Gln | Asn | Asn | Ala | His | Arg | Asp | Lys | Glu | Gly | Asp | Asp | Gln | Ser | His | Trp |      |
| 72  |     | 90  |     |     |     |     | 95  |     |     |     |     | 100 |     |     |     |     |      |
| 74  | cgc | tat | gga | ggc | gac | ccg | ccc | tgg | ccc | cgg | gtg | tcc | cca | gcc | tgc | gcg | 483  |
| 75  | Arg | Tyr | Gly | Gly | Asp | Pro | Pro | Trp | Pro | Arg | Val | Ser | Pro | Ala | Cys | Ala |      |
| 76  | 105 |     |     |     |     | 110 |     |     |     | 115 |     |     |     |     | 120 |     |      |
| 78  | ggc | cgc | ttc | cag | tcc | ccg | gtg | gat | atc | cgc | ccc | cag | ctc | gcc | gcc | ttc | 531  |
| 79  | Gly | Arg | Phe | Gln | Ser | Pro | Val | Asp | Ile | Arg | Pro | Gln | Leu | Ala | Ala | Phe |      |
| 80  |     |     |     | 125 |     |     |     |     | 130 |     |     |     |     | 135 |     |     |      |
| 82  | tgc | ccg | gcc | ctg | cgc | ccc | ctg | gaa | ctc | ctg | ggc | ttc | cag | ctc | ccg | ccg | 579  |
| 83  | Cys | Pro | Ala | Leu | Arg | Pro | Leu | Glu | Leu | Leu | Gly | Phe | Gln | Leu | Pro | Pro |      |
| 84  |     |     | 140 |     |     |     |     | 145 |     |     |     | 150 |     |     |     |     |      |
| 86  | ctc | cca | gaa | ctg | cgc | ctg | cgc | aac | aat | ggc | cac | agt | gtg | caa | ctg | acc | 627  |
| 87  | Leu | Pro | Glu | Leu | Arg | Leu | Arg | Asn | Asn | Gly | His | Ser | Val | Gln | Leu | Thr |      |
| 88  |     |     | 155 |     |     |     |     | 160 |     |     |     | 165 |     |     |     |     |      |
| 90  | ctg | cct | cct | ggg | cta | gag | atg | gct | ctg | ggg | ccc | ggg | cgg | gag | tac | cgg | 675  |
| 91  | Leu | Pro | Pro | Gly | Leu | Glu | Met | Ala | Leu | Gly | Pro | Gly | Arg | Glu | Tyr | Arg |      |
| 92  |     | 170 |     |     |     | 175 |     |     |     | 180 |     |     |     |     |     |     |      |
| 94  | gct | ctg | cag | ctg | cat | ctg | cac | tgg | ggg | gct | gca | ggg | cgt | ccg | ggc | tgc | 723  |
| 95  | Ala | Leu | Gln | Leu | His | Leu | His | Trp | Gly | Ala | Ala | Gly | Arg | Pro | Gly | Ser |      |
| 96  | 185 |     |     |     |     | 190 |     |     |     | 195 |     |     |     |     | 200 |     |      |
| 98  | gag | cac | act | gtg | gaa | ggc | cac | cgt | ttc | cct | gcc | gag | atc | cac | gtg | gtt | 771  |
| 99  | Glu | His | Thr | Val | Glu | Gly | His | Arg | Phe | Pro | Ala | Glu | Ile | His | Val | Val |      |
| 100 |     |     |     | 205 |     |     |     |     | 210 |     |     |     |     | 215 |     |     |      |
| 102 | cac | ctc | agc | acc | gcc | ttt | gcc | aga | gtt | gac | gag | gcc | ttg | ggg | cgc | ccg | 819  |
| 103 | His | Leu | Ser | Thr | Ala | Phe | Ala | Arg | Val | Asp | Glu | Ala | Leu | Gly | Arg | Pro |      |
| 104 |     |     | 220 |     |     |     |     | 225 |     |     |     |     | 230 |     |     |     |      |
| 106 | gga | ggc | ctg | gcc | gtg | ttg | gcc | gcc | ttt | ctg | gag | gag | ggc | ccg | gaa | gaa | 867  |
| 107 | Gly | Gly | Leu | Ala | Val | Leu | Ala | Ala | Phe | Leu | Glu | Glu | Gly | Pro | Glu | Glu |      |
| 108 |     |     | 235 |     |     |     |     | 240 |     |     |     |     | 245 |     |     |     |      |
| 110 | aac | agt | gcc | tat | gag | cag | ttg | ctg | tct | cgc | ttg | gaa | gaa | atc | gct | gag | 915  |
| 111 | Asn | Ser | Ala | Tyr | Glu | Gln | Leu | Leu | Ser | Arg | Leu | Glu | Glu | Ile | Ala | Glu |      |
| 112 |     | 250 |     |     |     | 255 |     |     |     | 260 |     |     |     |     |     |     |      |
| 114 | gaa | ggc | tca | gag | act | cag | gtc | cca | gga | ctg | gac | ata | tct | gca | ctc | ctg | 963  |
| 115 | Glu | Gly | Ser | Glu | Thr | Gln | Val | Pro | Gly | Leu | Asp | Ile | Ser | Ala | Leu | Leu |      |
| 116 | 265 |     |     |     |     | 270 |     |     |     | 275 |     |     |     |     | 280 |     |      |
| 118 | ccc | tct | gac | ttc | agc | cgc | tac | ttc | caa | tat | gag | ggg | tct | ctg | act | aca | 1011 |
| 119 | Pro | Ser | Asp | Phe | Ser | Arg | Tyr | Phe | Gln | Tyr | Glu | Gly | Ser | Leu | Thr | Thr |      |
| 120 |     |     |     | 285 |     |     |     |     | 290 |     |     |     |     | 295 |     |     |      |
| 122 | ccg | ccc | tgt | gcc | cag | ggg | gtc | atc | tgg | act | gtg | ttt | aac | cag | aca | gtg | 1059 |
| 123 | Pro | Pro | Cys | Ala | Gln | Gly | Val | Ile | Trp | Thr | Val | Phe | Asn | Gln | Thr | Val |      |
| 124 |     |     | 300 |     |     |     |     | 305 |     |     |     |     | 310 |     |     |     |      |
| 126 | atg | ctg | agt | gct | aag | cag | ctc | cac | acc | ctc | tct | gac | acc | ctg | tgg | gga | 1107 |
| 127 | Met | Leu | Ser | Ala | Lys | Gln | Leu | His | Thr | Leu | Ser | Asp | Thr | Leu | Trp | Gly |      |

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TIME: 13:48:40

Input Set : A:\USSN 09-807,949-SEQ LISTING.txt

Output Set: N:\CRF4\11232005\I807949C.raw

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128          315          320          325
130 cct ggt gac tct cgg cta cag ctg aac ttc cga gcg acg cag cct ttg 1155
131 Pro Gly Asp Ser Arg Leu Gln Leu Asn Phe Arg Ala Thr Gln Pro Leu
132          330          335          340
134 aat ggg cga gtg att gag gcc tcc ttc cct gct gga gtg gac agc agt 1203
135 Asn Gly Arg Val Ile Glu Ala Ser Phe Pro Ala Gly Val Asp Ser Ser
136 345          350          355          360
138 cct cgg gct gct gag cca gtc cag ctg aat tcc tgc ctg gct gct ggt 1251
139 Pro Arg Ala Ala Glu Pro Val Gln Leu Asn Ser Cys Leu Ala Ala Gly
140          365          370          375
142 gac atc cta gcc ctg gtt ttt ggc ctc ctt ttt gct gtc acc agc gtc 1299
143 Asp Ile Leu Ala Leu Val Phe Gly Leu Leu Phe Ala Val Thr Ser Val
144          380          385          390
146 gcg ttc ctt gtg cag atg aga agg cag cac aga agg gga acc aaa ggg 1347
147 Ala Phe Leu Val Gln Met Arg Arg Gln His Arg Arg Gly Thr Lys Gly
148          395          400          405
150 ggt gtg agc tac cgc cca gca gag gta gcc gag act gga gcc 1389
151 Gly Val Ser Tyr Arg Pro Ala Glu Val Ala Glu Thr Gly Ala
152          410          415          420
154 tagaggctgg atcttgagaga atgtgagaag ccagccagag gcatctgagg gggagccggg 1449
156 aactgtcctg tcctgtcat tatgccactt ccttttaact gccaaagaaat tttttaaaat 1509
158 aaatatttat aat 1522
161 <210> SEQ ID NO: 2
162 <211> LENGTH: 459
163 <212> TYPE: PRT
164 <213> ORGANISM: HUMAN
166 <400> SEQUENCE: 2
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168          -35          -30          -25
170 Pro Ala Pro Gly Leu Thr Val Gln Leu Leu Leu Ser Leu Leu Leu Leu
171          -20          -15          -10
173 Met Pro Val His Pro Gln Arg Leu Pro Arg Met Gln Glu Asp Ser Pro
174          -5          -1 1          5          10
176 Leu Gly Gly Gly Ser Ser Gly Glu Asp Asp Pro Leu Gly Glu Glu Asp
177          15          20          25
179 Leu Pro Ser Glu Glu Asp Ser Pro Arg Glu Glu Asp Pro Pro Gly Glu
180          30          35          40
182 Glu Asp Leu Pro Gly Glu Glu Asp Leu Pro Gly Glu Glu Asp Leu Pro
183          45          50          55
185 Glu Val Lys Pro Lys Ser Glu Glu Glu Gly Ser Leu Lys Leu Glu Asp
186          60          65          70          75
188 Leu Pro Thr Val Glu Ala Pro Gly Asp Pro Gln Glu Pro Gln Asn Asn
189          80          85          90
191 Ala His Arg Asp Lys Glu Gly Asp Asp Gln Ser His Trp Arg Tyr Gly
192          95          100          105
194 Gly Asp Pro Pro Trp Pro Arg Val Ser Pro Ala Cys Ala Gly Arg Phe
195          110          115          120
197 Gln Ser Pro Val Asp Ile Arg Pro Gln Leu Ala Ala Phe Cys Pro Ala
198          125          130          135

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200 Leu Arg Pro Leu Glu Leu Leu Gly Phe Gln Leu Pro Pro Leu Pro Glu
201 140 145 150 155
203 Leu Arg Leu Arg Asn Asn Gly His Ser Val Gln Leu Thr Leu Pro Pro
204 160 165 170
206 Gly Leu Glu Met Ala Leu Gly Pro Gly Arg Glu Tyr Arg Ala Leu Gln
207 175 180 185
209 Leu His Leu His Trp Gly Ala Ala Gly Arg Pro Gly Ser Glu His Thr
210 190 195 200
212 Val Glu Gly His Arg Phe Pro Ala Glu Ile His Val Val His Leu Ser
213 205 210 215
215 Thr Ala Phe Ala Arg Val Asp Glu Ala Leu Gly Arg Pro Gly Gly Leu
216 220 225 230 235
218 Ala Val Leu Ala Ala Phe Leu Glu Glu Gly Pro Glu Glu Asn Ser Ala
219 240 245 250
221 Tyr Glu Gln Leu Leu Ser Arg Leu Glu Glu Ile Ala Glu Glu Gly Ser
222 255 260 265
224 Glu Thr Gln Val Pro Gly Leu Asp Ile Ser Ala Leu Leu Pro Ser Asp
225 270 275 280
227 Phe Ser Arg Tyr Phe Gln Tyr Glu Gly Ser Leu Thr Thr Pro Pro Cys
228 285 290 295
230 Ala Gln Gly Val Ile Trp Thr Val Phe Asn Gln Thr Val Met Leu Ser
231 300 305 310 315
233 Ala Lys Gln Leu His Thr Leu Ser Asp Thr Leu Trp Gly Pro Gly Asp
234 320 325 330
236 Ser Arg Leu Gln Leu Asn Phe Arg Ala Thr Gln Pro Leu Asn Gly Arg
237 335 340 345
239 Val Ile Glu Ala Ser Phe Pro Ala Gly Val Asp Ser Ser Pro Arg Ala
240 350 355 360
242 Ala Glu Pro Val Gln Leu Asn Ser Cys Leu Ala Ala Gly Asp Ile Leu
243 365 370 375
245 Ala Leu Val Phe Gly Leu Leu Phe Ala Val Thr Ser Val Ala Phe Leu
246 380 385 390 395
248 Val Gln Met Arg Arg Gln His Arg Arg Gly Thr Lys Gly Gly Val Ser
249 400 405 410
251 Tyr Arg Pro Ala Glu Val Ala Glu Thr Gly Ala
252 415 420

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256 &lt;210&gt; SEQ ID NO: 3

257 &lt;211&gt; LENGTH: 29

258 &lt;212&gt; TYPE: DNA

259 &lt;213&gt; ORGANISM: HUMAN

261 &lt;400&gt; SEQUENCE: 3

262 cgcccagtgg gtcattctcc ccagaagag

29

265 &lt;210&gt; SEQ ID NO: 4

266 &lt;211&gt; LENGTH: 19

267 &lt;212&gt; TYPE: DNA

268 &lt;213&gt; ORGANISM: HUMAN

270 &lt;400&gt; SEQUENCE: 4

271 ggaatcctcc tgcattccgg

19

274 &lt;210&gt; SEQ ID NO: 5

## RAW SEQUENCE LISTING

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Input Set : A:\USSN 09-807,949-SEQ LISTING.txt

Output Set: N:\CRF4\11232005\I807949C.raw

275 <211> LENGTH: 10898  
 276 <212> TYPE: DNA  
 277 <213> ORGANISM: HUMAN  
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 280 <221> NAME/KEY: gene  
 281 <222> LOCATION: (1)..(10898)  
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 284 <220> FEATURE:  
 W--> 285 <221> NAME/KEY: unsure of base at position 1974  
 286 <222> LOCATION: (1974)  
 287 <223> OTHER INFORMATION: unsure of base at position 1974, which is in the 5' region  
 flanking the transcription initiation site (3507) as determined by RNase protection assay.  
 289 <400> SEQUENCE: 5  
 290 ggatcctgtt gactcgtgac cttacccccca accctgtgct ctctgaaaca tgagctgtgt 60  
 291 ccactcaggg ttaaatggat taagggcggt gcaagatgtg ctttggttaa cagatgcttg 120  
 292 aaggcagcat gctcgttaag agtcattacc aatcccta ctcaagtaat cagggacaca 180  
 293 aacactgagg aaggccgcag ggtcctctgc ctaggaaaac cagagacctt tgttcacttg 240  
 294 tttatctgac cttccctcca ctattgtcca tgaccctgcc aaatccccct ctgtgagaaa 300  
 295 caccacaaga ttatcaataa aaaaataaat taaaaaaaaa aatacaaaaa aaaaaaaaaa 360  
 296 aaaaaaaaaa gacttacgaa tagttattga taaatgaata gctattggta aagccaagta 420  
 297 aatgatcata ttcaaaacca gacggccatc atcacagctc aagtctacct gatttgatct 480  
 298 ctttatcatt gtcattcttt ggattcacta gatttagtcat catcctcaaa attctcccc 540  
 299 aagttctaata tacgttccaa acatttaggg gttacatgaa gcttgaacct actaccttct 600  
 300 ttgcttttga gccatgagtt gtaggaatga tgagtttaca ccttacatgc tggggattaa 660  
 301 tttaaacttt acctctaagt cagttgggta gcctttgggt tatttttgta gctaattttg 720  
 302 tagttaatgg atgcactgtg aatcttgcta tgatagtttt cctccacact ttgccactag 780  
 303 gggtaggtag gtactcagtt ttcagtaatt gcttacctaa gaccctaagc cctatttctc 840  
 304 ttgtactggc ctttatctgt aatatgggca tatttaatac aatataattt ttggagtttt 900  
 305 tttgtttgtt tgtttgtttg tttttttgag acggagtctt gcatctgtca tgcccaggct 960  
 306 ggagtagcag tggtgccatc tcggctcact gcaagctcca cctcccgagt tcacgccatt 1020  
 307 ttctgctc agcctccga gtagctggga ctacaggcgc ccgccaccat gcccggttaa 1080  
 308 ttttttgtat ttttggtaga gacggggttt caccgtgtta gccagaatgg tctcgatctc 1140  
 309 ctgacttctg gatccaccgc cctcggcctc ccaaagtctt gggattacag gtgtgagcca 1200  
 310 cgcacactgg ccaatttttt gagtctttta aagtaaaaat atgtcttgta agctggtaac 1260  
 311 tatggtacat ttctttttat taatgtggtg ctgacggtca tataggttct tttgagtttg 1320  
 312 gcatgcatat gctacttttt gcagtccttt cattacattt ttctctcttc atttgaagag 1380  
 313 catgttatat ctttttagctt cacttggttt aaaagggttt ctcattagcc taacacagtg 1440  
 314 tcattgttgg taccacttgg atcataagt gaaaaacagt caagaaattg cacagtaata 1500  
 315 cttgttttga agagggatga ttcaggtgaa tctgacacta agaaactccc ctacctgagg 1560  
 316 tctgagattc ctctgacatt gctgtatata ggcttttctt ttgacagcct gtgactgcgg 1620  
 317 actatttttc ttaagcaaga tatgctaaag ttttgtgagc ctttttccag agagaggtct 1680  
 318 catattctga tcaagtgaga acatataatg tctgcatgtt tccatatttc aggaattgtt 1740  
 319 gcttgtgttt tatgtcttta tatagacagg gaaacttgtt cctcagtgac ccaaaagagg 1800  
 320 tgggaattgt tattggatat catcattggc ccacgcttct tgaccttggg aacaattaa 1860  
 321 ggttcataat ctcaattctg tcagaattgg tacaagaaat agctgctatg tttcttgaca 1920  
 W--> 322 ttccacttgg taggaaataa gaatgtgaaa ctcttcagtt ggtgtgtgtc cctngttttt 1980  
 323 ttgcaatttc cttcttactg tgttaaaaaa aagtatgata ttgctctgag aggtgaggca 2040  
 324 ttcttaataca tgatctttta agatcaataa tataatcctt tcaaggatta tgtctttatt 2100  
 325 ataataaaga taatttgtct ttaacagaat caataatata atcccttaa ggattatatc 2160  
 326 tttgctgggc gcagtggctc acacctgtaa tcccagcact ttgggtggcc aaggtggaag 2220

RAW SEQUENCE LISTING ERROR SUMMARY  
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Input Set : A:\USSN 09-807,949-SEQ LISTING.txt  
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**Please Note:**

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:5; N Pos. 1974  
Seq#:25; Xaa Pos. 3,4  
Seq#:26; Xaa Pos. 3,4  
Seq#:58; N Pos. 1968  
Seq#:90; N Pos. 1968  
Seq#:110; N Pos. 647

**Invalid Line Length:**

The rules require that a line not exceed 72 characters in length. This includes spaces.

Seq#:5; Line(s) 287  
Seq#:9; Line(s) 521  
Seq#:25; Line(s) 698,704  
Seq#:26; Line(s) 719,724  
Seq#:58; Line(s) 1362,1368,1369  
Seq#:90; Line(s) 1803,1809,1810  
Seq#:110; Line(s) 2093,2099

**VERIFICATION SUMMARY**

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Input Set : A:\USSN 09-807,949-SEQ LISTING.txt

Output Set: N:\CRF4\11232005\I807949C.raw

L:11 M:270 C: Current Application Number differs, Replaced Current Application Number  
L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
L:285 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:5  
L:322 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5 after pos.:1920  
L:519 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:9  
L:702 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:25  
L:707 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:25 after pos.:0  
L:722 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:26  
L:727 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:26 after pos.:0  
L:1366 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:58  
L:1404 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:58 after pos.:1920  
L:1801 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:90  
L:1807 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:90  
L:1845 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:90 after pos.:1920  
L:2097 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:110  
L:2113 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:110 after pos.:600